

Initial assembled sequence  
[Strand]

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1   AGAAAATACC CACTTTCTCA GGATGATATC AATGGAATCC AGTCCATCTA TGGAGGTCTG
61  CCTAAGGAAC CTGCTAAGCC AAAGGAACCC ACTATACCCG ATGCCTGTGA CCCTGACTTG
121 ACTTTTGACG CTATCACAAC TTTCCGCAGA GAAGTAATGT TCTTTAAAGG CAGGCACCTA
181 TGGAGGATCT ATTATGATAT CACGGATGTT GAGTTTGAAT TAATTGCTTC ATTCTGGCCA
241 TCTCTGCCAG CTGATCTGCA AGCTGCATAC GAGAACCCCA GAGATAAGAT TCTGGTTTTT
301 AAAGATGAAA ACTTCTGGAT GATCAGAGGA TATGCTGTCT TGCCAGATTA TCCCAAATCC
361 ATCCATACAT TAGGTTTTTC AGGACGTGTG AAGAAAATAG ATGCAGCCGT CTGTGATAAG
421 ACCACAAGAA AAACCTACTT CTTTGTGGGC ATTTGGTGCT GGAGGTTTGA TGAAATGACC
481 CAAACCATGG ACAAAGGGTT CCCGCAGAGA GTGGTAAAC ACTTTCCTGG AATCAGTATC
541 CGTGTTGATG CTGCTTTCCA GTACAAAGGA TTCTTCTTTT TCAGCCGTGG ATCAACGCAA
601 TTTGAATACG ACATTAAGAC AAAGAATATT ACCCGAATCA TGAGAACTAA TACTTGGTTT
661 CAATGCAAAG AACCAGAGAA CTCCTCATTT GGTTTGTATA TCAACAAGGA AAAAGCACAT
721 TCAGGAGGCA TAAAGATATT GTATCATAAG AGTTTAAGCT TGTTTATTTT TGGTATTGTT
781 CATTTGCTGA AAAACACTTC TATTTATCAA TAAATTCATA GACCTAAAAT AAA

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Figure 1

gaaagagagg a	atg aag cgc ctt ctg ctt ctg ttt ttg ttc ttt ata aca	50
	<u>Met Lys Arg Leu Leu Leu Leu Phe Leu Phe Phe Ile Thr</u>	
	1 5 10	
ttt tct tct gca ttt ccc tta gtc cgg atg atg gaa aat gaa gaa aat	98	
<u>Phe Ser Ser</u> Ala Phe Pro Leu Val Arg Met Met Glu Asn Glu Glu Asn		
15 20 25		
gtg caa ctg gct cag gca tat ctc aac cag ttc tac tct ctt gaa ata	146	
Val Gln Leu Ala Gln Ala Tyr Leu Asn Gln Phe Tyr Ser Leu Glu Ile		
30 35 40 45		
gaa ggg aat cat ctt gtt caa agc aag aat agg agt ctc ata gat gac	194	
Glu Gly Asn His Leu Val Gln Ser Lys Asn Arg Ser Leu Ile Asp Asp		
50 55 60		
aaa att cgg gaa atg caa gca ttt ttt gga ttg aca gtg act gga aga	242	
Lys Ile Arg Glu Met Gln Ala Phe Phe Gly Leu Thr Val Thr Gly Arg		
65 70 75		
ctg gac tca aac acc ctt gag atc atg aag aca <u>ccc agg tgt ggg gtg</u>	290	
Leu Asp Ser Asn Thr Leu Glu Ile Met Lys Thr <u>Pro Arg Cys Gly Val</u>		
80 85 90		
<u>cct gat</u> gtg ggc cag tat ggc tac acc ctc cct ggg tgg aga aaa tac	338	
<u>Pro Asp</u> Val Gly Gln Tyr Gly Tyr Thr Leu Pro Gly Trp Arg Lys Tyr		
95 100 105		
aac ctc acc tac aga ata ata aac tat act ccg gat atg gca cga gct	386	
Asn Leu Thr Tyr Arg Ile Ile Asn Tyr Thr Pro Asp Met Ala Arg Ala		
110 115 120 125		
gct gtg gat gag gct atc caa gaa ggt tta gaa gtg tgg agc aaa gtc	434	
Ala Val Asp Glu Ala Ile Gln Glu Gly Leu Glu Val Trp Ser Lys Val		
130 135 140		
act cca cta aaa ttc acc aag att tca aag ggg att gca gac atc atg	482	
Thr Pro Leu Lys Phe Thr Lys Ile Ser Lys Gly Ile Ala Asp Ile Met		
145 150 155		
att gcc ttt agg act cga gtc cat ggt cgg tgt cct cgc tat ttt gat	530	
Ile Ala Phe Arg Thr Arg Val His Gly Arg Cys Pro Arg Tyr Phe Asp		
160 165 170		
ggt ccc ttg gga gtt ctt ggc cat gcc ttt cct cct ggt ccg ggt ctg	578	
Gly Pro Leu Gly Val Leu Gly His Ala Phe Pro Pro Gly Pro Gly Leu		
175 180 185		
ggt ggt gac act cat ttt gat gag gat gaa aac tgg acc aag gat gga	626	
Gly Gly Asp Thr His Phe Asp Glu Asp Glu Asn Trp Thr Lys Asp Gly		
190 195 200 205		
gca gga ttc aac ttg ttt ctt gtg gct gct cat gaa ttt ggt cat gca	674	
Ala Gly Phe Asn Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ala		
210 215 220		

**Figure 2A**

ctg ggg ctc tct cac tcc aat gat caa aca gcc ttg atg ttc cca aat Leu Gly Leu Ser His Ser Asn Asp Gln Thr Ala Leu Met Phe Pro Asn 225 230 235	722
tat gtc tcc ctg gat ccc aga aaa tac cca ctt tct cag gat gat atc Tyr Val Ser Leu Asp Pro Arg Lys Tyr Pro Leu Ser Gln Asp Asp Ile 240 245 250	770
aat gga atc cag tcc atc tat gga ggt ctg cct aag gaa cct gct aag Asn Gly Ile Gln Ser Ile Tyr Gly Gly Leu Pro Lys Glu Pro Ala Lys 255 260 265	818
cca aag gaa ccc act ata ccc cat gcc tgt gac cct gac ttg act ttt Pro Lys Glu Pro Thr Ile Pro His Ala Cys Asp Pro Asp Leu Thr Phe 270 275 280 285	866
gac gct atc aca act ttc cgc aga gaa gta atg ttc ttt aaa ggc agg Asp Ala Ile Thr Thr Phe Arg Arg Glu Val Met Phe Phe Lys Gly Arg 290 295 300	914
cac cta tgg agg atc tat tat gat atc acg gat gtt gag ttt gaa tta His Leu Trp Arg Ile Tyr Tyr Asp Ile Thr Asp Val Glu Phe Glu Leu 305 310 315	962
att gct tca ttc tgg cca tct ctg cca gct gat ctg caa gct gca tac Ile Ala Ser Phe Trp Pro Ser Leu Pro Ala Asp Leu Gln Ala Ala Tyr 320 325 330	1010
gag aac ccc aga gat aag att ctg gtt ttt aaa gat gaa aac ttc tgg Glu Asn Pro Arg Asp Lys Ile Leu Val Phe Lys Asp Glu Asn Phe Trp 335 340 345	1058
atg atc aga gga tat gct gtc ttg cca gat tat ccc aaa tcc atc cat Met Ile Arg Gly Tyr Ala Val Leu Pro Asp Tyr Pro Lys Ser Ile His 350 355 360 365	1106
aca tta ggt ttt cca gga cgt gtg aag aaa ata gat gca gcc gtc tgt Thr Leu Gly Phe Pro Gly Arg Val Lys Lys Ile Asp Ala Ala Val Cys 370 375 380	1154
gat aag acc aca aga aaa acc tac ttc ttt gtg ggc att tgg tgc tgg Asp Lys Thr Thr Arg Lys Thr Tyr Phe Phe Val Gly Ile Trp Cys Trp 385 390 395	1202
agg ttt gat gaa atg acc caa acc atg gac aaa ggg ttc ccg cag aga Arg Phe Asp Glu Met Thr Gln Thr Met Asp Lys Gly Phe Pro Gln Arg 400 405 410	1250
gtg gta aaa cac ttt cct gga atc agt atc cgt gtt gat gct gct ttc Val Val Lys His Phe Pro Gly Ile Ser Ile Arg Val Asp Ala Ala Phe 415 420 425	1298
cag tac aaa gga ttc ttc ttt ttc agc cgt gga tca acg caa ttt gaa Gln Tyr Lys Gly Phe Phe Phe Phe Ser Arg Gly Ser Thr Gln Phe Glu 430 435 440 445	1346

**Figure 2B**

tac gac att aag aca aag aat att acc cga atc atg aga act aat act	1394
Tyr Asp Ile Lys Thr Lys Asn Ile Thr Arg Ile Met Arg Thr Asn Thr	
450 455 460	
tggttt caa tgc aaa gaa cca aag aac tcc tca ttt ggt ttt gat atc	1442
Trp Phe Gln Cys Lys Glu Pro Lys Asn Ser Ser Phe Gly Phe Asp Ile	
465 470 475	
aac aag gaa aaa gca cat tca gga ggc ata aag ata ttg tat cat aag	1490
Asn Lys Glu Lys Ala His Ser Gly Gly Ile Lys Ile Leu Tyr His Lys	
480 485 490	
agt tta agc ttg ttt att ttt ggt att gtt cat ttg ctg aaa aac act	1538
Ser Leu Ser Leu Phe Ile Phe Gly Ile Val His Leu Leu Lys Asn Thr	
495 500 505	
tct att tat caa taaattcata gacctaaaat aaacctcaac aggtctttta	1590
Ser Ile Tyr Gln	
510	
atataaaattc tgcttcaaaa tagaataaaa ccattcttta acaacaagtt gctgggtccta	1650
gttctaaata tccaaattca atggccattt tgagctgcoct gattctttta ataggaagtt	1710
attatgtaga aacaaaaatc tctgactgta ctttaagcoct atttcatgct ttgtggactt	1770
ggagaagaca tgtcttataa ctgaatactg aaacatttat <u>taa</u> accaatc ttttagcattc	1830
tg	1832

**Figure 2C**

Figure 3

[illegible]

Second Zn<sup>2+</sup> and Ca<sup>2+</sup> binding domain

[illegible]Zn<sup>2+</sup> binding domain[illegible]

	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583
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423	DAAPYK-HY	FTS62570FENIXDXTOTLDTOT	FTF002P	ES579FD00000000000	ELYNKSLFT	751110000000	TYO	contg 353 long
424	Y-HDD	Y-FH TR YKP P	R. LITAKA. S	N. PCK				contg 353 short
425	Y-HDD	HYFS PRYAF LQART	TA. G. K	LY NIG				COLLUM 780
426	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
427	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
428	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
429	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
430	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
431	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
432	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
433	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
434	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
435	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
436	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
437	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
438	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
439	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
440	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
441	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
442	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
443	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
444	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
445	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
446	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
447	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
448	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
449	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
450	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
451	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
452	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
453	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
454	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
455	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
456	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
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458	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
459	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
460	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
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462	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
463	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
464	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
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466	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
467	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
468	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780
469	Y-HDD	Y-FH PI	S WSKN. P	PA. S	ILW			COLLUM 780

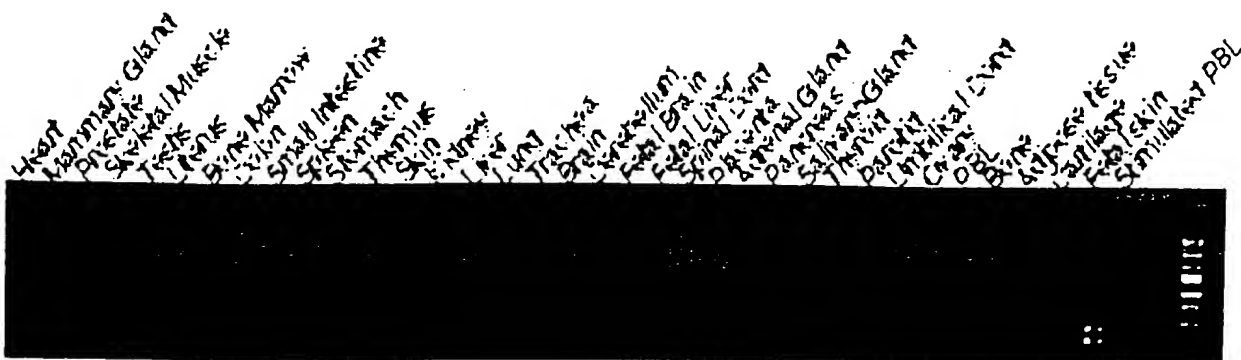
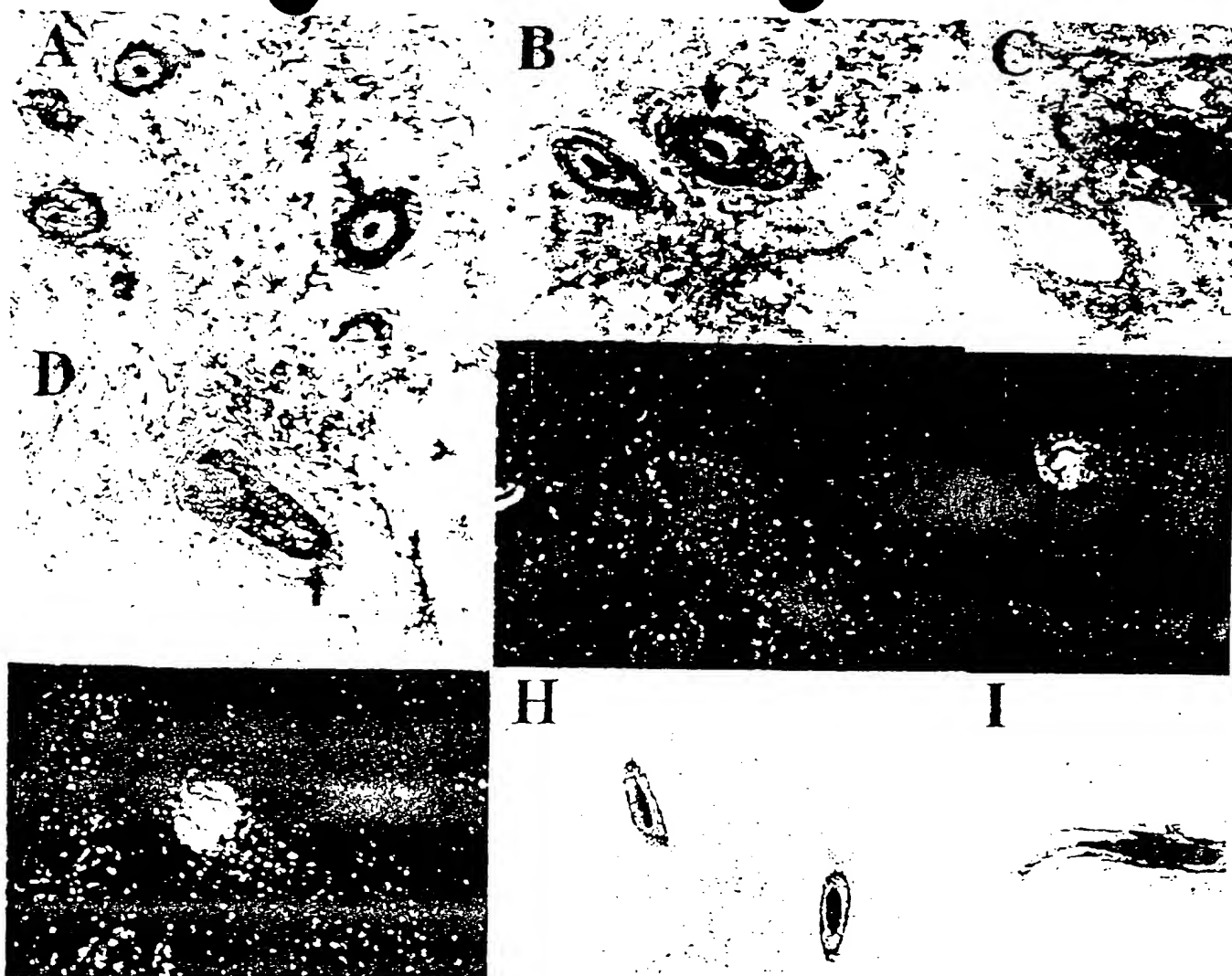


Figure 4



A-G: Antisense RNA probe for human MMP 25

H and I: Sense RNA probe for human MMP 25

Arrows in A, B, C, and D highlight cells in the hair follicle that express MMP25 message

Cell nuclei are counterstained with H33258 in E, F, and G.

Figure 5